

Amendments to the Specification

Please amend page 8, lines 1 to 6 as follows:

Figure 12 compares the nucleotide sequence of a control duplex (SEQ ID NO:1 and SEQ ID NO:2) with the aptamer domain of the analyte sensor of Figure 11 (SEQ ID NO: 3 and SEQ ID NO: 4) (showing two bound adenosines). The extent of the aptamer domain is indicated (shown as boxed), with the two bound adenosines shown as outlined 'A' s. "D" and "P" indicate guanine doublets distally and proximally located, respectively, relative to the covalently conjugated anthraquinone (AQ) moiety.

Please amend page 9, lines 4-11 as follows:

Figure 15 (a) shows the structure and sequence of the "coupled-ligand" sensor (SEQ ID NO: 5, SEQ ID NO: 6, and SEQ ID NO: 7). The ATP aptamer domain is indicated as boxed, while the two bound adenosines are indicated by outlined 'A's. Guanine doublets in the 5' -32P-end labeled strand used to monitor charge transfer to the Sensor and Detector stems are indicated as "x", "y", and "z". The AoG mismatch at the junction was used since it gave superior results relative to Watson-Crick base pairs at that position. The arrow, on an adenine at the junction, indicates an adenine that showed an unusually high cleavage (see Figure 15 (b), lane 4, below).

Please amend the specification by adding the following text at the end of the specification, beginning at line 1 of a new page 42:

SEQUENCE LISTING

<110> Simon Fraser University

<120> DNA AND RNA CONFORMATIONAL SWITCHES AS SENSITIVE ELECTRONIC SENSORS OF ANALYTES

<130> S168 0173/TWB

<140> 10/507,837

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